Introduction to Proteomics—Tools for the New Biology

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Anyone involved in mass spectrometry these days will be at least vaguely familiar with the term proteomics whether or not they have direct involvement studying the proteome. For those who need a good introduction, Dr. Dan Liebler has written a wonderful introductory book on this subject.

The book is well organized and gives good coverage of the topic. It is divided into three sections. The first section describes proteomics. The second section describes the tools that are used to study proteomics, and the third section covers applications. All of the tables and figures used throughout the book are well done and offer excellent visual assistance to the text. Many terms used in proteomics are defined throughout the book such as, "mining," "spot trains," "peak parking," and "shotgun." This book is concise and informative.

The first section is an overview to the way biology is now being studied. It describes the relationship of the proteome with the genome.

The second section of the book, the tools needed to study proteomics, covers sample preparation, mass spectrometers, mass spec techniques and databases. The first chapters in this section describe working with complex mixtures to prepare the samples for digestion. It includes the use of subcellular fractionation, 1-D and 2-D gel electrophoresis, isoelectric focusing, and HPLC to prepare samples for digestion into peptides. Why and how to digest a protein into peptides is then discussed. Chapter six is devoted to description of the mass spectrometers with most of the emphasis on the MALDI and ESI sources and three types of tandem analyzers. The analyzers discussed include the triple quadrupole, the ion trap, and the quadrupole-time of flight. Many terms are defined and defined well. Unfortunately one mistake did escape the authors proofing. In his description of a time-of flight analyzer, he describes the speed of an ion traveling the flight tube and says "the greater the m/z the faster they fly," when it is the smaller ions that will travel the tube the fastest. This should not be viewed as a reason not to read this book. The benefits far outweigh this mistake.

The next chapters go on to describe how the peptides generated in the digest are analyzed by mass spectrometry. Chapter 7 describes analysis and software used in peptide mass fingerprinting, and Chapter 8 describes sequencing. The last chapters of Section II discuss the database analysis of the data obtained. The description of the databases was a bit disappointing for me. The author goes into detail describing Sequest and Salsa, but I do not have access to either. Because a good understanding of how the databases work is my weak point, I would really have liked to have seen a more in-depth description of all the more commonly used databases.

The third section of the book describes how these techniques can be applied to mining the proteome, monitoring changes in proteins and their interactions with other proteins, and mapping modifications of proteins. The author compares mining approaches, introduces software packages for 2-D gel analysis, and isotopic tagging and talks about antibodies and the "bait" approach for capturing a protein.

Each chapter ends with suggested readings and the book offers more than 60 references to some of the more recent advances in proteomics as well as the classic beginnings.

This book would be an excellent addition to the library of someone intending to learn proteomics. It is descriptive but to the point. It is a blend of biology for the mass spectrometrist and mass spectrometry for the biologist. This is not an easy mix. I find it hard to believe that anyone, even those already well versed in proteomics, could read this book and not learn something new. I would challenge anyone to walk away having read this book and not feel that they have been introduced to proteomics and feel confident that they have a good basic understanding of this new and exciting field.

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